Elsevier has created a Monkeypox Information Center in response to the declared public health emergency of international concern, with free information in English on the monkeypox virus. The Monkeypox Information Center is hosted on Elsevier Connect, the company's public news and information website.

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antifungal therapy (12 months) rather than prolonged. The results of our study suggest that 12 months of oral itraconazole is better than 6 months of itraconazole. Any treatment for chronic pulmonary aspergillosis beyond 12 months should generally be in the context of a clinical trial.

We declare no competing interests

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Tracking the 2022 monkeypox outbreak with epidemiological data in real-time

Monkeypox virus was first documented in humans in the 1970s and outbreaks have been reported in many countries, with most cases restricted to endemic areas.[1] In early May, 2022, monkeypox cases were reported in the UK, Spain, and elsewhere in Europe (figure, appendix).[2] The pattern of geographical dispersal was much larger compared with past outbreaks that were more localised and occurred often in under-resourced communities.[3] The size of the outbreak clusters is growing each day, as is the geographical spread across Europe and North America. Within the first week of the initial report, 24 countries reported suspected and confirmed cases of monkeypox virus, some of which had known travel links to the UK, Spain, Canada, and western Europe. As of June 5, 2022, there have been 920 confirmed and 70 suspected cases. Of 64 confirmed cases with known travel history, 32 were associated with travel from Europe, three from west Africa, two from Canada, and one from Australia. For 26 cases, travel history locations remain unknown.

WHO convened a meeting of experts and technical advisory groups on May 20, 2022,[4] to investigate the causes of the outbreak and have released updated guidance on surveillance, case investigation, and contact tracing.[5] The reason for the outbreak having a broader geographical reach is being investigated by the international and national public health community and the research community, contributing to a finer scale understanding of the outbreak dynamics. However, cessation of smallpox vaccination programmes, encroachment of humans into forested areas, and growing international mobility seem to be playing important roles in the epidemiology of monkeypox virus outbreaks.[6]

To support global response efforts, our team created an open-access database and visualisation to track the occurrence of cases in different countries. In addition, where available, we added information on age (aggregated into age ranges, with a minimum range of 5 years), gender, dates of symptom onset and laboratory confirmation, symptoms, locations (aggregated to the state level), travel history, and additional metadata defined by WHO.[5]

Data are compiled from verified sources, including reports from governments and public health organisations and news media reporting of health official statements. As verified information and official statements are published, we document secondary sources and update the metadata in the dataset. An on-call schedule for curators that runs 24 h a day, 7 days a week was established to ensure data are updated in near real-time. Each case is seen and discussed by at least two curators before being made available via our Global.health GitHub repository, and pushed to the map visualisation at least four times per day.

During the early stages of outbreaks, obtaining reliable, synthesised data on the characteristics of cases is a challenge, especially at a global scale. Our work attempts to harmonise information across countries and provide additional data to support the epidemiological understanding of the origins and transmission dynamics of this outbreak. Ideally, these data are paired with virus genomic data and integrated directly with countries' epidemiological line-list data. In our repository, we are also working with colleagues and the WHO Hub for Pandemic and Epidemic Intelligence to define a contact data schema allowing countries and researchers to estimate and re-estimate key epidemiological parameters, such as the incubation period and serial interval, across different settings.

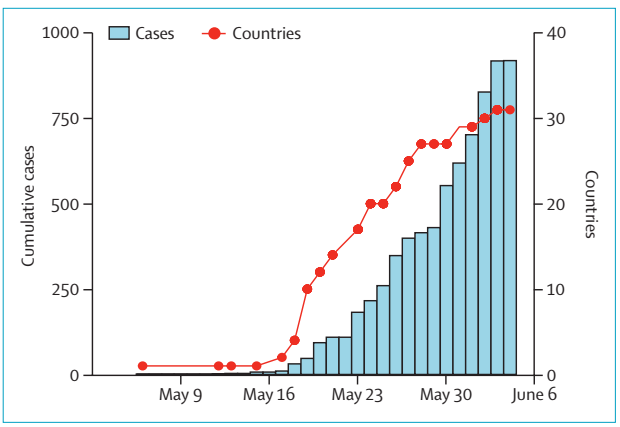

Figure: **Rapid expansion of the 2022 monkeypox outbreak**
Cumulative number of confirmed cases (by confirmation date) since the first reported case in the 2022 outbreak, and cumulative number of countries reporting confirmed cases.

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See **Online** for appendix

For more on the **Global.health open-access database on monkeypox** see https://github.com/globaldothealth/monkeypox/blob/main/latest.csv

For more on the **monkeypox outbreak tracker** see https://map.monkeypox.global.health/country

For more on our **Global.health GitHub repository** see https://github.com/globaldothealth/monkeypox

Real-time data are necessary to plan effective control measures should this outbreak grow further. The work builds on infrastructure developed for epidemic control and pandemic preparedness and was used for the COVID-19 pandemic.[7] Global efforts are needed to ensure similar efforts to rapidly harmonise and publish detailed epidemiological data are supported during future outbreaks of emerging and re-emerging pathogens. This example will be a learning pathway to build better surveillance systems globally.

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See **Online** for appendix

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Neutralisation sensitivity of SARS-CoV-2 omicron subvariants to therapeutic monoclonal antibodies

During the current pandemic, SARS-CoV-2 has considerably diversified. The omicron variant (B.1.1.529) was identified at the end of November, 2021, and rapidly spread worldwide. As of May, 2022, the omicron BA.2 subvariant is the most dominant variant in the world. Other omicron subvariants have since emerged and some of them have begun to outcompete BA.2 in multiple countries. For instance, omicron BA.2.11 subvariant is spreading in France, and the BA.2.12.1 and BA.4/5 subvariants are becoming dominant in the USA and South Africa, respectively (appendix pp 4–5).

Newly emerging SARS-CoV-2 variants need to be carefully monitored for a potential increase in transmission rate, pathogenicity, and resistance to immune responses. The resistance of variants to vaccines and therapeutic antibodies can be attributed to a variety of mutations in the viral spike protein. Although the spike proteins of new omicron subvariants (BA.2.11, BA.2.12.1, and BA.4/5) are derived from the BA.2 spike protein, the majority of them additionally bear the following mutations in the spike: BA.2.11, L452R; BA.2.12.1, L452Q and S704L; and BA.4/5, L452R, HV69-70del, F486V, and R493Q (appendix pp 4–5). In particular, the L452R and L452Q substitutions were detected in the delta (B.1.617.2) and lambda (C.37) variants, respectively, and we demonstrated that the L452R/Q substitution affects sensitivity to vaccine-induced neutralising antibodies.[1,2] Therefore, it is reasonable to assume that these new omicron subvariants have reduced sensitivity to therapeutic monoclonal antibodies. To address this possibility, we generated pseudoviruses harbouring the spike proteins of these omicron subvariants and derivatives and prepared eight therapeutic monoclonal antibodies (appendix pp 2–3). Consistent with previous studies,[3–5] bamlanivimab, casirivimab, etesevimab, imdevimab, and tixagevimab were less functional against BA.2 than the parental virus (table). These five antibodies were also less functional against new omicron subvariants, whereas the BA.2 spike bearing the R493Q substitution was partially sensitive to casirivimab and tixagevimab (table; appendix pp 4–5). Bebtelovimab was approximately 2-fold more effective against BA.2 and all omicron subvariants tested than the parental virus (table). Although sotrovimab was roughly 20-fold less effective against BA.2 than the parental virus, the omicron subvariants bearing the L452R substitution, including BA.2.11 and BA.4/5, were more sensitive to sotrovimab than BA.2 (table). Evusheld (cilgavimab and tixagevimab), particularly cilgavimab, was effective against BA.2, whereas